

Amendments to the Claims:

This listing of claims will replace all prior versions, and listings, of claims in the application:

Listing of Claims:

1. (Currently Amended) A method for ~~obtaining~~ storing DNA fingerprint ~~profile~~ data, comprising the steps of:
~~measuring peak intensity and size of each DNA fragment in a sample of genomic DNA;~~
(a) providing a DNA fingerprint comprising resolved labeled DNA markers and a DNA size standard that are labeled to emit a detectable signal;
(b) detecting the signals emitted from said labeled DNA markers and measuring the peak intensity and location of said signals;
(c) determining the size of said labeled DNA markers by comparison with said DNA size standard;
(d) classifying the peak ~~intensities~~ intensity of said ~~fragments~~ signals emitted from said labeled DNA markers according to a predetermined discrete intensity level scale;
(e) aligning the sizes of said ~~fragments~~ labeled DNA markers into corresponding ones of discrete size bins that have a value that correlates to a base pair number;
~~determining a sequence of fragments according to values of said bins;~~
~~entering the classified peak intensities of said fragments into a data record in said sequence; and~~
(f) creating a data record, wherein the step of creating the data record comprises, for each labeled DNA marker, associating a value with the labeled DNA marker wherein the value corresponds to the classified peak intensity of the signal emitted from said labeled DNA marker and entering the value into the data record at a predetermined location within the data record, wherein the location of each said value within the data record is a function of the size of the labeled DNA marker with which the value is associated; and

(g) storing the said data record.

2. (Currently Amended) The method of claim 1, wherein said sample DNA fingerprint is ~~obtained by AFLP~~ an amplified fragment length polymorphism DNA fingerprint.

3. (Currently Amended) The method of claim 1, wherein said sample DNA fingerprint is ~~obtained by RFLP~~ a restriction fragment length polymorphism DNA fingerprint.

4. (Currently Amended) The method of claim 1, wherein said sample DNA fingerprint is ~~obtained by SSR-PCR~~ a simple sequence repeats polymerase chain reaction DNA fingerprint.

5. (Currently Amended) The method of claim 1, wherein said sample DNA fingerprint is ~~obtained by VNTR-PCR~~ a variable number tandem repeats polymerase chain reaction DNA fingerprint.

6. (Currently Amended) The method of claim 1, further comprising the step of normalizing the measured peak intensities of said ~~fragments~~ DNA marker signals before ~~classifying said peak intensities according to said discrete intensity level scale~~ (d).

7. (Currently Amended) The method of claim 6, 1, wherein said discrete intensity level scale comprises at least five discrete peak levels.

8. (Currently Amended) The method of claim 1, wherein the step of aligning comprises the steps of:

grouping ~~fragment~~ DNA marker sequences of said ~~fragments~~ DNA markers into clusters, wherein adjacent peaks of each cluster are less than or equal to a predetermined number of discrete positions apart;

assigning a potential energy value to each cluster, said potential energy value being proportional to the spacing between adjacent peaks of the cluster and to the amount of displacement required to bin the peaks into discrete size bins;

varying the displacement of said peaks so that said potential energy value is minimized; and

aligning said peaks into discrete size bins according to the displacement values that result in a minimized potential energy value.

9. (Currently Amended) The method of claim 1, wherein ~~said step of entering (g)~~ comprises the step of creating a data record having:

an information field including

an identification of the source of the ~~genomic~~ DNA fingerprint,

the ~~method type of producing DNA fragments from said source~~ fingerprint,

the spacing between successive ~~fragments~~ DNA markers,

the starting size of said ~~fragments~~ DNA markers, and

the ending size of said ~~fragments~~ DNA markers; and

a sequence field containing ~~a sequence of~~ said data record of the sequence of classified peak intensities of DNA marker signals.

10. (Original) The method of claim 9, further comprising the step of scoring a comparison between two data records, including the steps of assigning reward points to matches of peak intensities and penalty points to mismatches of peak intensities, based on the relative magnitude of said peak intensities, comparing said two data records for identical matches at corresponding size positions, comparing said two data records for identical matches at adjacent size positions, comparing said two data records for non-identical matches at corresponding size positions, and comparing said two data records for non-identical matches at adjacent size positions, and totaling said reward points and penalty points according to found matches and remaining mismatches to obtain a score.

11. (Original) The method of claim 10, further comprising the step of obtaining a

percentage metric for two compared data records, by obtaining a ratio of said score to a score obtained by matching one of said two data records to itself.

12. (Currently Amended) A computer program product, comprising:

a computer-readable medium having computer-executable code recorded thereon for ~~obtaining~~ storing DNA fingerprint ~~profile~~ data, said computer-executable code comprising:

means for ~~measuring~~ storing data corresponding to the peak intensity of the signal emitted by labeled DNA markers and the size of each DNA fragment marker in a sample of genomic DNA fingerprint;

means for classifying the peak intensities of said ~~fragments~~ signals emitted by labeled DNA markers according to a predetermined discrete intensity level scale;

means for aligning the sizes of said ~~fragments~~ labeled DNA markers into corresponding ones of discrete size bins;

~~means for determining a sequence of fragments according to values of said bins;~~

~~means for entering the classified peak intensities of said fragments into a data record in said sequence; and~~

means for creating a data record, wherein the means for creating the data record comprises: means for associating each labeled DNA marker with a value that corresponds to the classified peak intensity of the signal emitted from said labeled DNA marker and means for entering the values into the data record at predetermined locations within the data record, such that the location of each said value within the data record is a function of the size of the labeled DNA marker with which the value is associated; and

means storing ~~the~~ said data record in a computer-readable storage medium.

13. (Currently Amended) The computer program product of claim 12, further comprising:

means for normalizing the measured peak intensities of said ~~fragments~~ labeled DNA markers before classifying said peak intensities according to said discrete intensity level scale.

14. (Original) The computer program product of claim 13, wherein said discrete intensity level scale comprises at least five discrete peak levels.

15. (Currently Amended) The computer program product of claim 12, wherein said means for aligning comprises:

means for grouping ~~fragment~~ DNA marker sequences of said ~~fragments~~ DNA markers into clusters, wherein adjacent peaks of each cluster are less than or equal to a predetermined number of discrete positions apart;

means for assigning a potential energy value to each cluster, said potential energy value being proportional to the spacing between adjacent peaks of the cluster and to the amount of displacement required to bin the peaks into discrete size bins;

means for varying the displacement of said peaks so that said potential energy value is minimized; and

means for aligning said peaks into discrete size bins according to the displacement values that result in a minimized potential energy value.

16. (Currently Amended) The computer program product of claim 12, wherein said means for entering comprises means for creating a data record having:

an information field including

an identification of the source of the ~~genomic~~ DNA fingerprint,

the ~~method type~~ of ~~producing~~ DNA fragments from said source fingerprint,

the spacing between successive ~~fragments~~ DNA markers,

the starting size of said ~~fragments~~ DNA markers, and

the ending size of said ~~fragments~~ DNA markers; and

a sequence field containing ~~a sequence of~~ said data record of the sequence of classified peak intensities of DNA marker signals.

17. (Currently Amended) A computer system, comprising:

a computer; and

a computer-readable storage medium having a DNA fingerprint data record stored

therein, ~~said DNA fingerprint data including size and peak intensity of DNA fragments produced from a DNA sample obtained from a source of genomic DNA, wherein said DNA fingerprint was obtained from a genomic DNA source,~~ said data record comprising:

an information field including:

~~an identification of the source of~~ information identifying the genomic DNA from which the DNA fingerprint was obtained,

information identifying the method type of producing DNA fragments from said source fingerprint,

information identifying the spacing between successive fragments DNA markers,

information identifying the starting size of said fragments DNA markers, and

information identifying the ending size of said fragments DNA markers; and

a sequence field containing a sequence of ~~said classified transformed DNA marker signal~~ peak intensity symbols,

wherein ~~when said storage medium is coupled to a computer and said~~ said computer is programmed to read said data record is read from said storage medium by said computer,
~~said computer converts and convert~~ said sequence of classified transformed DNA marker signal peak intensity symbols into a unique DNA fingerprint record identifying a specific trait of unique to said source of genomic DNA source identified in said information field.